

Identification of Genetic Module Associated with Trichome Development in Cotton

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Abstract

In *Gossypium arboreum*, we established a regulatory network involving five genes *GaHD1*, *GaHDG11*, *GaZHD2*, *GaCPR5*, and *GaSMR3* by using in vivo and in vitro molecular biology approaches (Fig.1). Furthermore, phenotypic analysis at cellular, tissue, and organ levels in transgenic plants through Overexpressing or Knocking out the *GaZHD2*, *GaCPR5*, and *GaSMR3* elucidated the mechanistic role of these genes in controlling cotton trichome development.

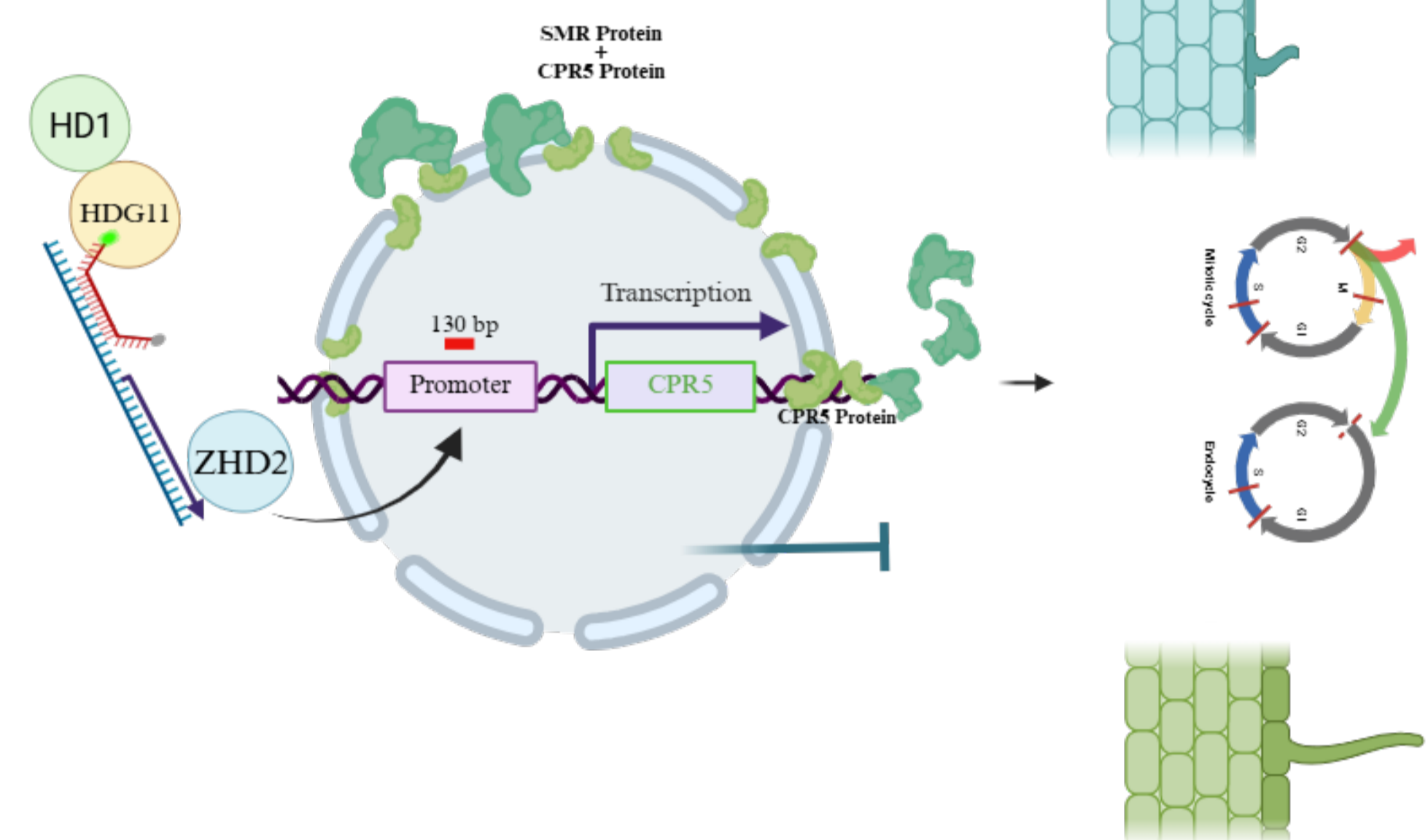


Fig.1 Hypothesis of *GaHD1-GaHDG11-GaZHD2-GaCPR5-GaSMR3* module in regulating trichomes elongation in cotton

Introduction

Cotton trichomes are mainly distributed on the surface of seed, leaf and stem. The trichomes with different structures are involved in response to abiotic and biotic stress (Fig.2). Cotton leaf and stem surface trichomes are similar to cotton fiber in structure, and the development process is regulated by genes related to fiber development (Fig.3). In all wild cotton species, the phenotype of long trichome can be only observed in A genome species. As the donor of A genome of tetraploid cultivars, wild species and cultivated species of A genome are important materials for studying the molecular regulation mechanism related to trichome elongation.

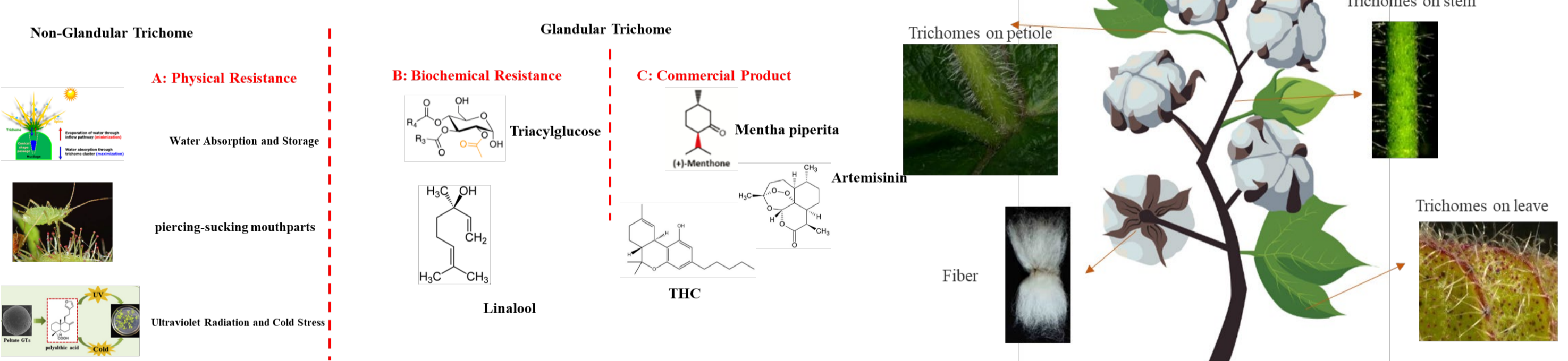


Fig.2 Trichomes function in biotic and abiotic stress

Fig.3 Cotton trichomes in different organs

Methodology

Molecular Mechanisms Regulating Cotton Trichomes

Transcriptomes of *GaCPR5* knockout lines, overexpression lines, and wild-type plants will be sequenced and comparatively analyzed to identify differentially expressed genes. The upstream regulators of *GaCPR5* was validated by using Y1H assays, Dual-LUC, and DAP-seq. Y2H will be employed to identify *GaCPR5*-interacting proteins, which will be further validated BiFC, and pull-down assays.

Identification and Function Analysis of Candidate Genes for Trichome Elongation

Functional predictions of the candidate gene will be conducted using bioinformatics approaches, and the role of *GaCPR5* will be validated through phenotypic characterization of *GaCPR5* knockout and overexpression transgenic lines (Fig.4).

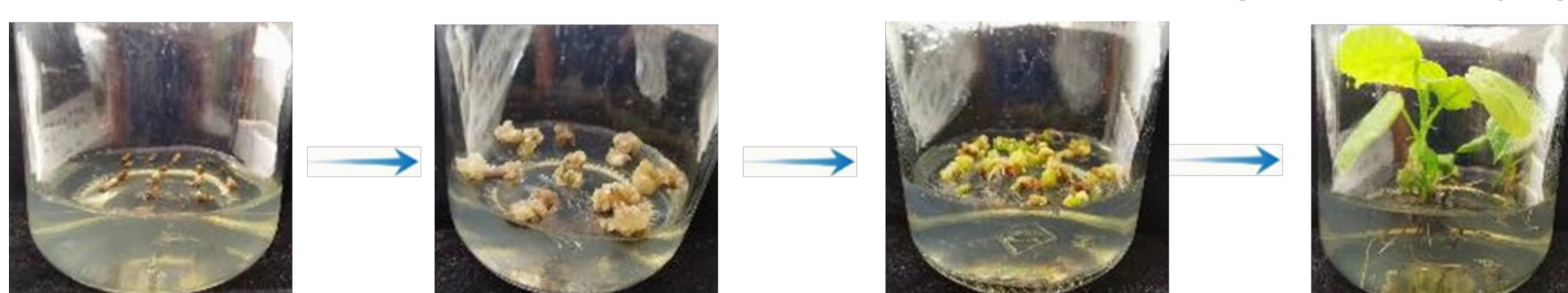


Fig.4 main steps in the cotton tissue culture process

Conclusion and Perspectives

This study aims to construct a regulatory network governing cotton trichome development, centered on the *GaCPR5* gene. To decipher the molecular mechanisms underlying cotton trichome development. To provide a theoretical foundation for understanding the development of cotton fibers, which share a similar cellular structure with trichomes.



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Main Results

- The *Gossypium* species which are distributed in the place near the low latitude generally are found high density trichomes.

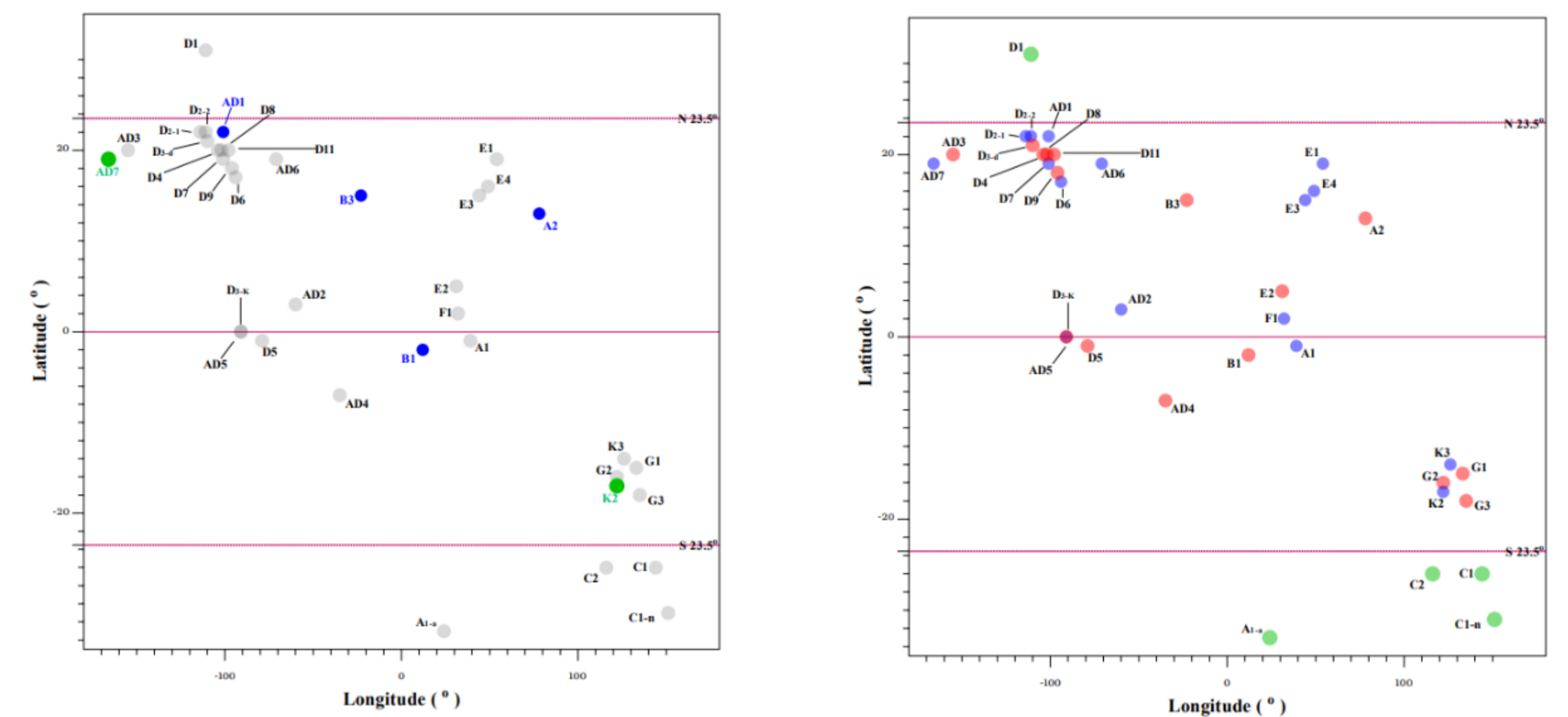


Fig.5 The distribution of *Gossypium* Species with Different Trichome Phenotype.

- Trichomes undergo specific elongation during the second true leaf stage.

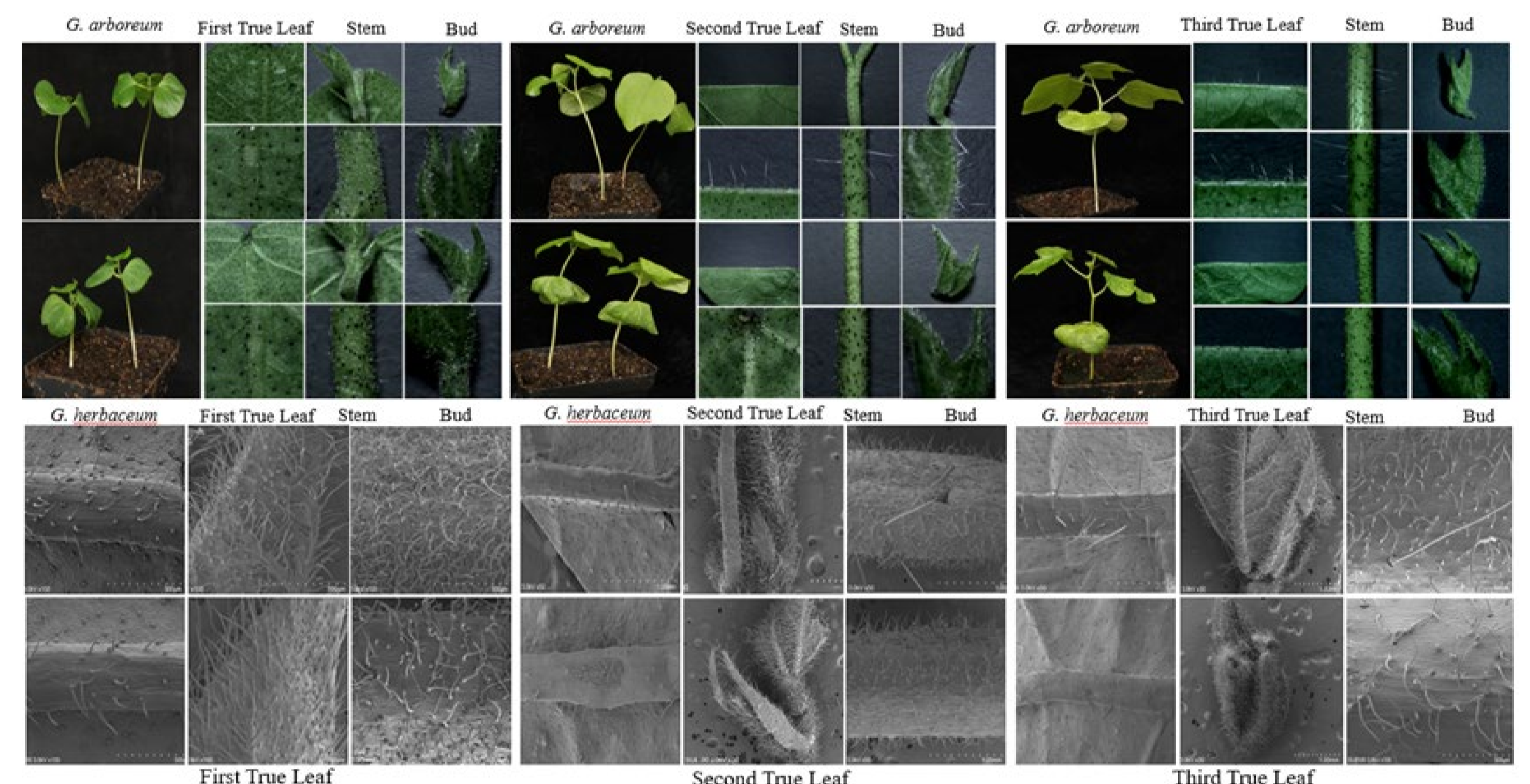


Fig.6 Trichomes development in *DY-10* on leaf, stem, bud in different development stages

- Identification of *GaHD1-GaHDG11-GaZHD2-GaCPR5-GaSMR3* module via Dual-Luc.

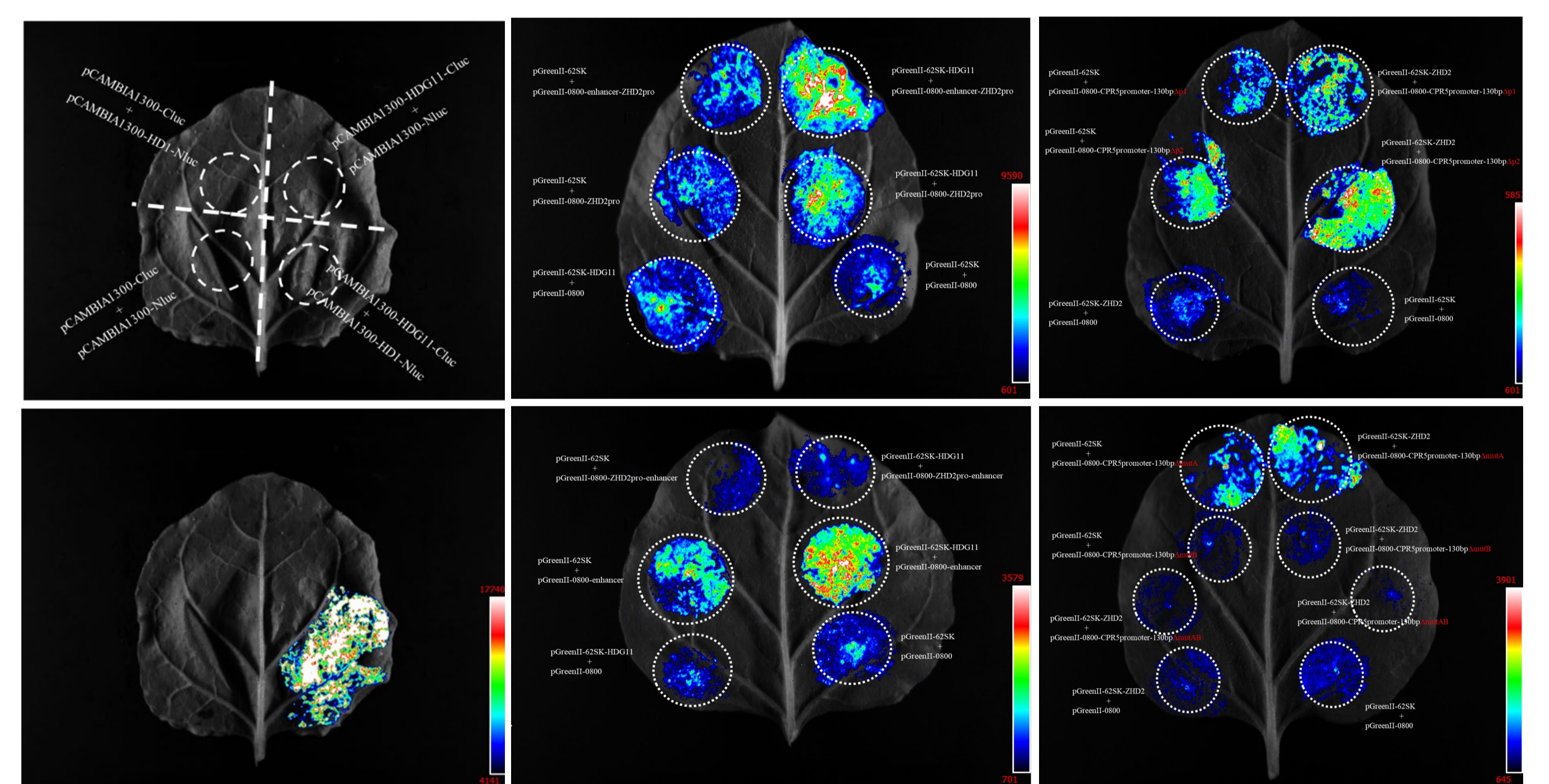


Fig.7 Genetic module construction via dual-luciferase reporter gene assays

- GaCPR5* Positively Regulates Trichome Elongation via Overexpression.

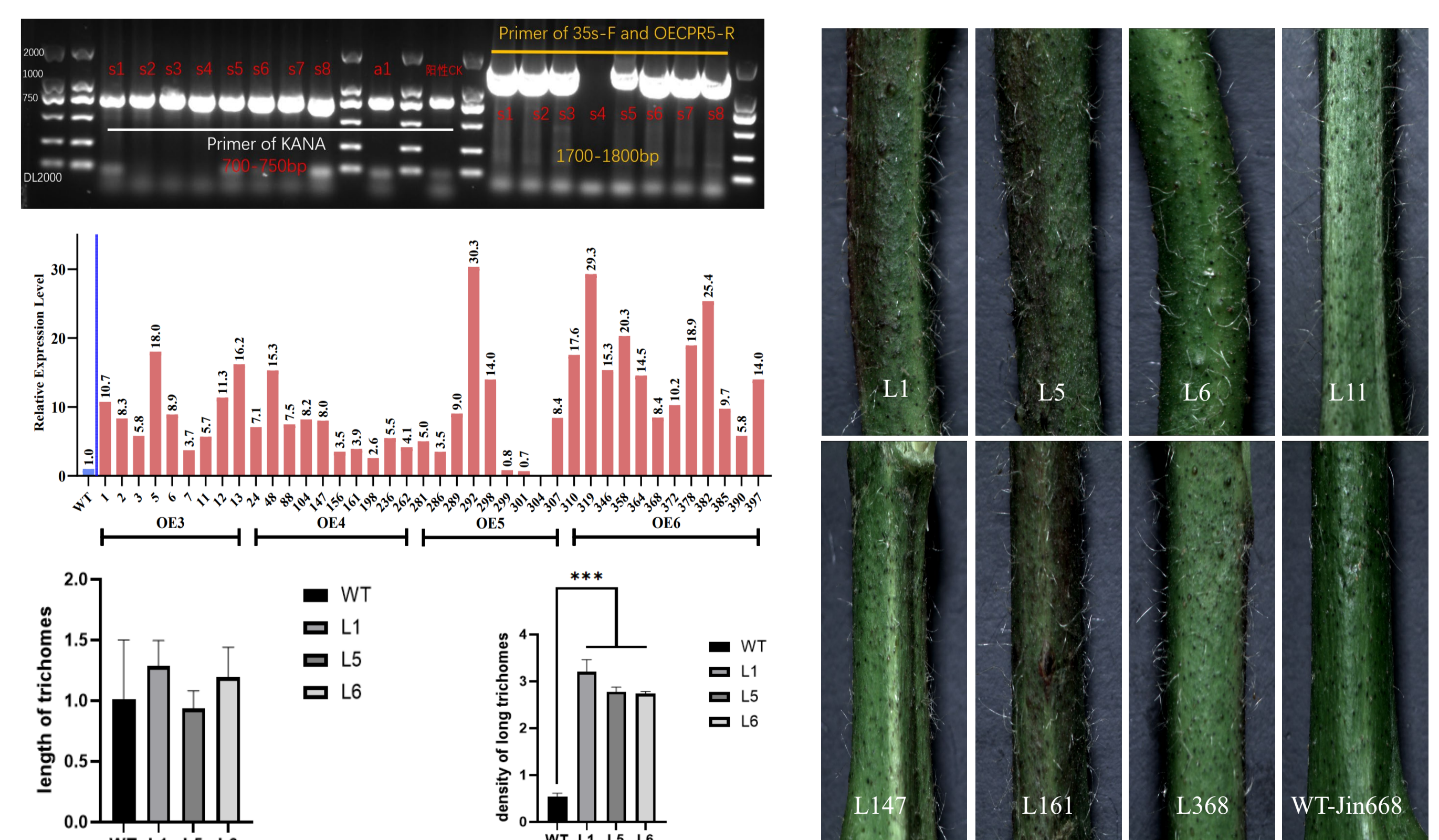


Fig.8 Construction and phenotype identification of *GaCPR5* overexpression lines

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